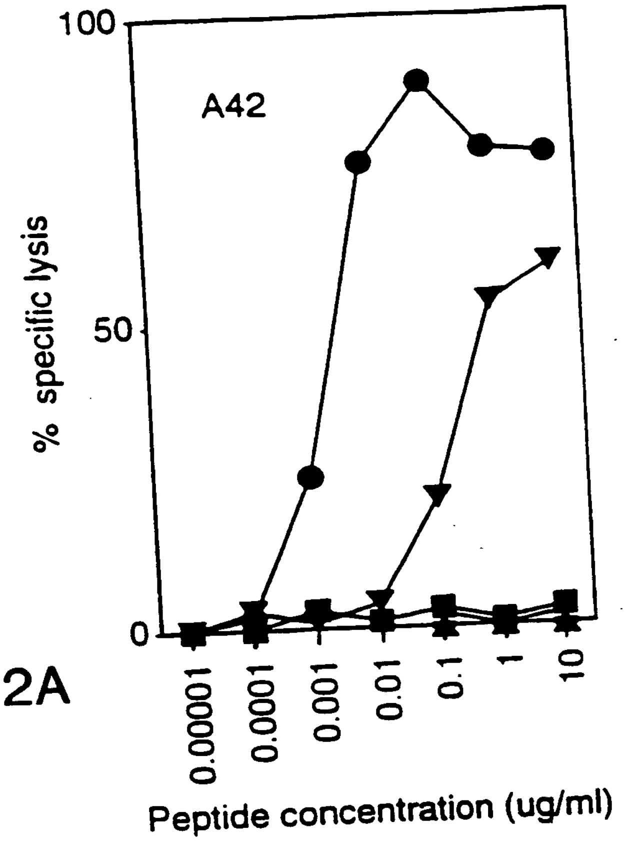
```
                                                                              59
1    AGCAGACAGAGGACTCTCATTAAGGAAGG TGTCCTGTGCCCTGACCCTACAAGATGCCA
                                                          MetPro              2

60   AGAGAAGATGCTCACTTCATCTATGGTTAC CCCAAGAAGGGGCACGGCCACTCTTACACC         119
3    ArgGluAspAlaHisPheIleTyrGlyTyr ProLysLysGlyHisGlyHisSerTyrThr          22

120  ACGGCTGAAGAGGCCGCTGGGATCGGCATC CTGACAGTGATCCTGGGAGTCTTACTGCTC         180
23   ThrAlaGluGluAlaAlaGlyIleGlyIle LeuThrValIleLeuGlyValLeuLeuLeu          43

181  ATCGGCTGTTGGTATTGTAGAAGACGAAAT GGATACAGAGCCTTGATGGATAAAAGTCTT         239
44   IleGlyCysTrpTyrCysArgArgArgAsn GlyTyrArgAlaLeuMetAspLysSerLeu          62

240  CATGTTGGCACTCAATGTGCCTTAACAAGA AGATGCCCACAAGAAGGGTTTGATCATCGG         300
63   HisValGlyThrGlnCysAlaLeuThrArg ArgCysProGlnGluGlyPheAspHisArg          83

301  GACAGCAAAGTGTCTCTTCAAGAGAAAAAC TGTGAACCTGTGGTTCCCAATGCTCCACCT         359
84   AspSerLysValSerLeuGlnGluLysAsn CysGluProValValProAsnAlaProPro         102

360  GCTTATGAGAAACTCTCTGCAGAACAGTCA CCACCACCTTATTCACCTTAAGAGCCAGCG         420
103  AlaTyrGluLysLeuSerAlaGluGlnSer ProProProTyrSerPro                     118

421  AGACACCTGAGACATGCTGAAATTATTTCT CTCACACTTTTGCTTGAATTTAATACAGAC         479
```

FIG. 1A

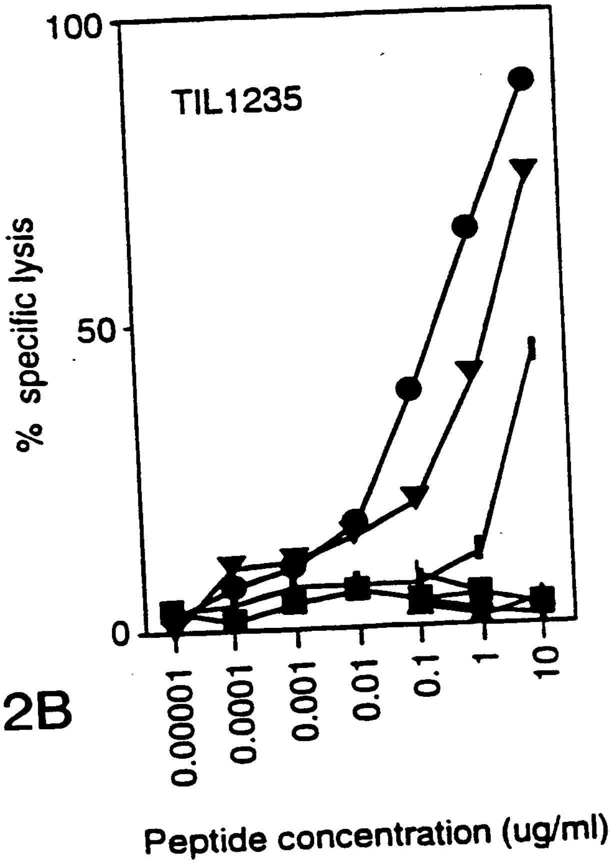
```
480   ATCTAATGTTCTCCTTTGGAATGGTGTAGG AAAAATGCAAGCCATCTCTAATAATAAGTC   540
541   AGTGTTAAAATTTTAGTAGGTCCGCTAGCA GTACTAATCATGTGAGGAAATGATGAGAAA   599
600   TATTAAATTGGGAAAACTCCATCAATAAAT GTTGCAATGCATGATACTATCTGTGCCAGA   660
661   GGTAATGTTAGTAAATCCATGGTGTTATTT TCTGAGAGACAGAATTCAAGTGGGTATTCT   719
720   GGGGCCATCCAATTTCTCTTTACTTGAAAT TTGGCTAATAACAAACTAGTCAGGTTTTCG   780
781   AACCTTGACCGACATGAACTGTACACAGAA TTGTTCCAGTACTATGGAGTGCTCACAAAG   839
840   GATACTTTTACAGGTTAAGACAAAGGGTTG ACTGGCCTATTTATCTGATCAAGAACATGT   900
901   CAGCAATGTCTCTTTGTGCTCTAAAATTCT ATTATACTACAATAATATATTGTAAAGATC   959
960   CTATAGCTCTTTTTTTTTGAGATGGAGTTT CGCTTTTGTTGCCCAGGCTGGAGTGCAATG  1020
1021  GCGCGATCTTGGCTCACCATAACCTCCGCC TCCCAGGTTCAAGCAATTCTCCTGCCTTAG  1079
1080  CCTCCTGAGTAGCTGGGATTACAGGCGTGC GCCACTATGCCTGACTAATTTTGTAGTTTT  1140
1141  AGTAGAGACGGGGTTTCTCCATGTTGGTCA GGCTGGTCTCAAACTCCTGACCTCAGGTGA  1199
1200  TCTGCCCGCCTCAGCCTCCCAAAGTGCTGG AATTACAGGCGTGAGCCACCACGCCTGGCT  1260
1261  GGATCCTATATCTTAGGTAAGACATATAAC GCAGTCTAATTACATTTCACTTCAAGGCTC  1319
1320  AATGCTATTCTAACTAATGACAAGTATTTT CTACTAAACCAGAAATTGGTAGAAGGATTT  1380
1381  AAATAAGTAAAAGCTACTATGTACTGCCTT AGTGCTGATGCCTGTGTACTGCCTTAAATG  1439
1440  TACCTATGGCAATTTAGCTCTCTTGGGTTC CCAAATCCCTCTCACAAGAATGTGCAGAAG  1500
1501  AAATCATAAAGGATCAGAGATTCTGAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAA   1559
```

FIG. 1B



100
50
0
A42
% specific lysis
0.00001
0.0001
0.001
0.01
0.1
1
10
Peptide concentration (ug/ml)

FIG. 2A



100
50
0
TIL1235
% specific lysis
0.00001
0.0001
0.001
0.01
0.1
1
10
Peptide concentration (ug/ml)

FIG. 2B

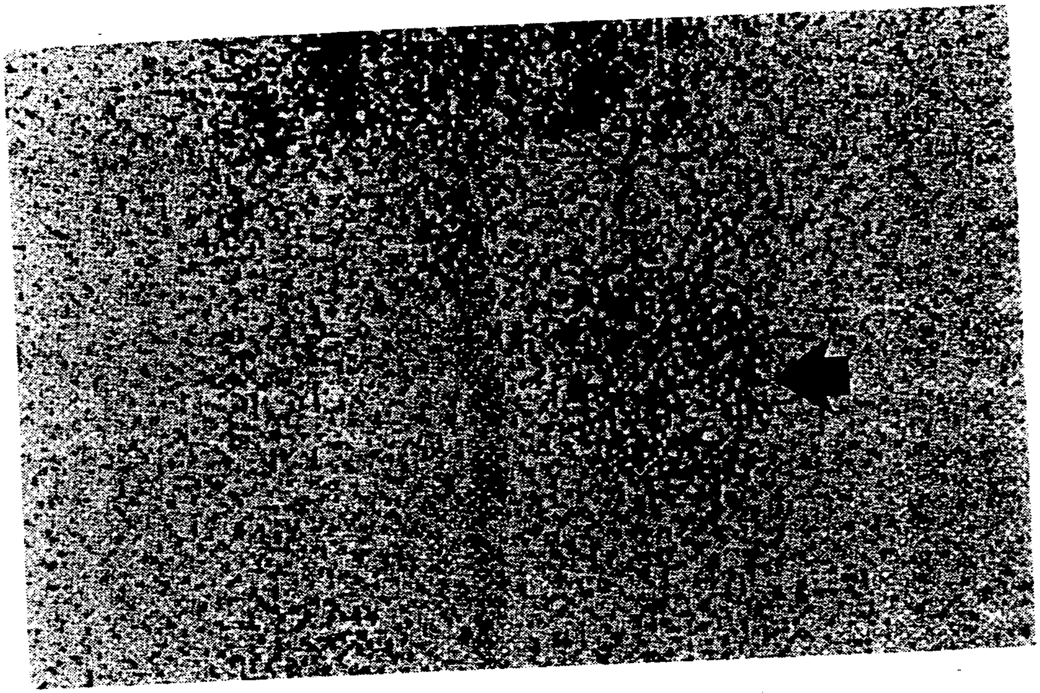


FIG. 3A

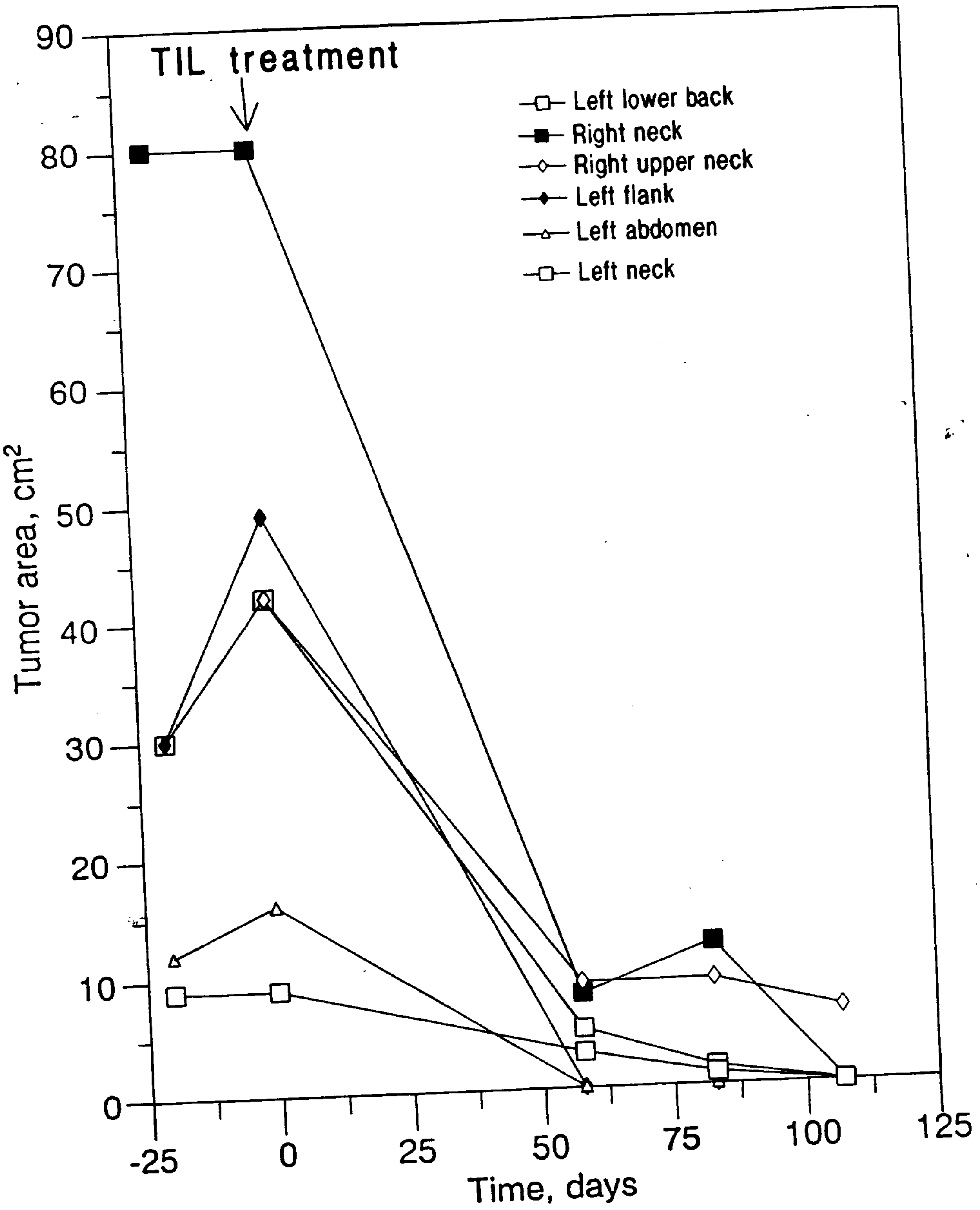

TIL treatment
Left lower back
Right neck
Right upper neck
Left flank
Left abdomen
Left neck
Tumor area, cm^2
Time, days
0
10
20
30
40
50
60
70
80
90
-25
0
25
50
75
100
125

FIG. 3B

GTCGACGGCC ATTACCAATC GCGACCGGGA AGAACACAAT 40

GGATCTGGTG CTAAAAAGAT GCCTTCTTCA TTTGGCTGTG 80

ATAGGTGCTT TGCTGGCTGT GGGGGCTACA AAAGTACCCA 120

GAAACCAGGA CTGGCTTGGT GTCTCAAGGC AACTCAGAAC 160

CAAAGCCTGG AACAGGCAGC TGTATCCAGA GTGGACAGAA 200

GCCCAGAGAC TTGACTGCTG GAGAGGTGGT CAAGTGTCCC 240

TCAAGGTCAG TAATGATGGG CCTACACTGA TTGGTGCAAA 280

TGCCTCCTTC TCTATTGCCT TGAACTTCCC TGGAAGCCAA 320

AAGGTATTGC CAGATGGGCA GGTTATCTGG GTCAACAATA 360

CCATCATCAA TGGGAGCCAG GTGTGGGGAG GACAGCCAGT 400

GTATCCCCAG GAAACTGACG ATGCCTGCAT CTTCCCTGAT 440

GGTGGACCTT GCCCATCTGG CTCTTGGTCT CAGAAGAGAA 480

GCTTTGTTTA TGTCTGGAAG ACCTGGGGCC AATACTGGCA 520

ATTTCTAGGG GGCCCAGTGT CTGGGCTGAG CATTGGGACA 560

GGCAGGGCAA TGCTGGGCAC ACACACCATG GAAGTGACTG 600

TCTACCATCG CCGGGGATCC CGGAGCTATG TGCCTCTTGC 640

TCATTCCAGC TCAGCCTTCA CCATTACTGA CCAGGTGCCT 680

TTCTCCGTGA GCGTGTCCCA GTTGCGGGCC TTGGATGGAG 720

GGAACAAGCA CTTCCTGAGA AATCAGCCTC TGACCTTTGC 760

CCTCCAGCTC CATGACCCCA GTGGCTATCT GGCTGAAGCT 800

GACCTCTCCT ACACCTGGGA CTTTGGAGAC AGTAGTGGAA 840

CCCTGATCTC TCGGGCACTT GTGGTCACTC ATACTTACCT 880

GGAGCCTGGC CCAGTCACTG CCCAGGTGGT CCTGCAGGCT 920

GCCATTCCTC TCACCTCCTG TGGCTCCTCC CCAGTTCCAG 960

GCACCACAGA TGGGCACAGG CCAACTGCAG AGGCCCCTAA 1000

CACCACAGCT GGCCAAGTGC CTACTACAGA AGTTGTGGGT 1040

ACTACACCTG GTCAGGCGCC AACTGCAGAG CCCTCTGGAA 1080

CCACATCTGT GCAGGTGCCA ACCACTGAAG TCATAAGCAC 1120

FIG. 4A

```
TGCACCTGTG CAGATGCCAA CTGCAGAGAG CACAGGTATG    1160
ACACCTGAGA AGGTGCCAGT TTCAGAGGTC ATGGGTACCA    1200
CACTGGCAGA GATGTCAACT CCAGAGGCTA CAGGTATGAC    1240
ACCTGCAGAG GTATCAATTG TGGTGCTTTC TGGAACCACA    1280
GCTGCACAGG TAACAACTAC AGAGTGGGTG GAGACCACAG    1320
CTAGAGAGCT ACCTATCCCT GAGCCTGAAG GTCCAGATGC    1360
CAGCTCAATC ATGTCTACGG AAAGTATTAC AGGTTCCCTG    1400
GGCCCCCTGC TGGATGGTAC AGCCACCTTA AGGCTGGTGA    1440
AGAGACAAGT CCCCCTGGAT TGTGTTCTGT ATCGATATGG    1480
TTCCTTTTCC GTCACCCTGG ACATTGTCCA GGGTATTGAA    1520
AGTGCCGAGA TCCTGCAGGC TGTGCCGTCC GGTGAGGGGG    1560
ATGCATTTGA GCTGACTGTG TCCTGCCAAG GCGGGCTGCC    1600
CAAGGAAGCC TGCATGGAGA TCTCATCGCC AGGGTGCCAG    1640
CCCCCTGCCC AGCGGCTGTG CCAGCCTGTG CTACCCAGCC    1680
CAGCCTGCCA GCTGGTTCTG CACCAGATAC TGAAGGGTGG    1720
CTCGGGGACA TACTGCCTCA ATGTGTCTCT GGCTGATACC    1760
AACAGCCTGG CAGTGGTCAG CACCCAGCTT ATCATGCCTG    1800
GTCAAGAAGC AGGCCTTGGG CAGGTTCCGC TGATCGTGGG    1840
CATCTTGCTG GTGTTGATGG CTGTGGTCCT TGCATCTCTG    1880
ATATATAGGC GCAGACTTAT GAAGCAAGAC TTCTCCGTAC    1920
CCCAGTTGCC ACATAGCAGC AGTCACTGGC TGCGTCTACC    1960
CCGCATCTTC TGCTCTTGTC CCATTGGTGA GAACAGCCCC    2000
CTCCTCAGTG GGCAGCAGGT CTGAGTACTC TCATATGATG    2040
CTGTGATTTT CCTGGAGTTG ACAGAAACAC CTATATTTCC    2080
CCCAGTCTTC CCTGGGAGAC TACTATTAAC TGAAATAAAT    2120
ACTCAGAGCC TGAAAAAAAA TAAAAAAAAA AAAAAAAAAA    2160
AAAAAAAAAA AA                                  2172
```

FIG. 4B

```
  1   MDLVLKRCLL HLAVIGALLA VGATKVPRNQ DWLGVSRQLR TKAWNRQLYP
 51   EWTEAQRLDC WRGGQVSLKV SNDGPTLIGA NASFSIALNF PGSQKVLPDG
101   QVIWVNNTII NGSQVWGGQP VYPQETDDAC IFPDGGPCPS GSWSQKRSFV
151   YVWKTWGQYW QFLGGPVSGL SIGTGRAMLG THTMEVTVYH RRGSRSYVPL
201   AHSSSAFTIT DQVPFSVSVS QLRALDGGNK HFLRNQPLTF ALQLHDPSGY
251   LAEADLSYTW DFGDSSGTLI SRALVVTHTY LEPGPVTAQV VLQAAIPLTS
301   CGSSPVPGTT DGHRPTAEAP NTTAGQVPTT EVVGTTPGQA PTAEPSGTTS
351   VQVPTTEVIS TAPVQMPTAE STGMTPEKVP VSEVMGTTLA EMSTPEATGM
401   TPAEVSIVVL SGTTAAQVTT TEWVETTARE LPIPEPEGPD ASSIMSTESI
451   TGSLGPLLDG TATLRLVKRQ VPLDCVLYRY GSFSVTLDIV QGIESAEILQ
501   AVPSGEGDAF ELTVSCQGGL PKEACMEISS PGCQPPAQRL CQPVLPSBAC
551   QLVLHQILKG GSGTYCLNVS LADTNSLAVV STQLIMPGQE AGLGQVPLIV
601   GILLVLMAVV LASLIYRRRL MKQDFSVPQL PHSSSHWLRL PRIFCSCPIG
651   ENSPLLSGQQ V
```

FIG. 5A

```
Pmel17      M-----V-----Q-----P-----VPGILLT-----LLSGQQV
ME20        M-----V-----Q-----L-----  ......-------------
gp100       M-----V-----Q-----L-----.......-------------
cDNA25FL    M-----F-----Q-----L-----.......-------------
cDNA25TR                Q-----L-----.......-----PPQWAAGLSTLI
            1     162   236   274   588         649
```

FIG. 5B

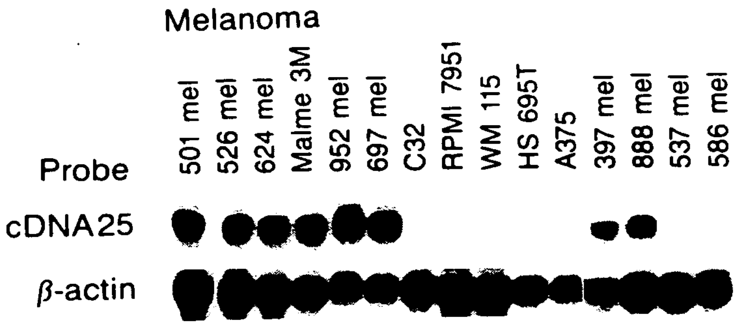


FIG. 6A

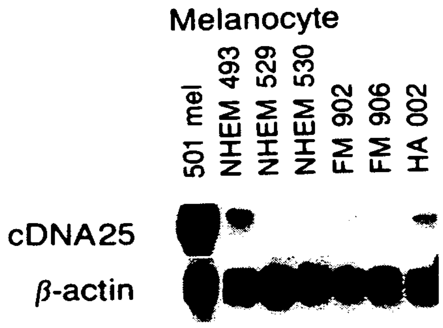


FIG. 6B

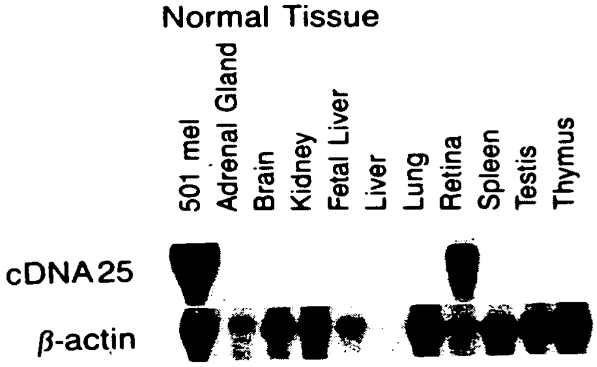


FIG. 6C